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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/899,303A

DATE: 11/23/2001

TIME: 18:16:03

Input Set : N:\Crf3\RULE60\09899303A.raw

Output Set: N:\CRF3\11232001\I899303A.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: MAERTENS, GEERT
 6 BOSMAN, FONS
 7 DE MARTYNOFF, GUY
 8 BUYSE, MARIE-ANGE

10 (ii) TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
 11 PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

13 (iii) NUMBER OF SEQUENCES: 111

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: NIXON & VANDERHYE P.C.
 17 (B) STREET: 1100 NORTH GLEBE ROAD
 18 (C) CITY: ARLINGTON
 19 (D) STATE: VIRGINIA
 20 (E) COUNTRY: U.S.A.
 21 (F) ZIP: 22201-4714

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk
 25 (B) COMPUTER: IBM PC compatible
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/899,303A
 C--> 31 (B) FILING DATE: 06-Jul-2001
 32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US/08/612,973
 36 (B) FILING DATE: 11-MAR-1996

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: BYRNE, THOMAS E.
 40 (B) REGISTRATION NUMBER: 32,205
 41 (C) REFERENCE/DOCKET NUMBER: 1487-10

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: (703) 816-4000
 45 (B) TELEFAX: (703) 816-4100

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 21 base pairs
 53 (B) TYPE: nucleic acid
 54 (C) STRANDEDNESS: single
 55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: cDNA

59 (iii) HYPOTHETICAL: NO

C--> 61 (iv) ANTI-SENSE: NO

66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

68 GGCATGCAAG CTTAATTAAT T

70 (2) INFORMATION FOR SEQ ID NO: 2:

ENTERED

21

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Input Set : N:\Crf3\RULE60\09899303A.raw
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72 (i) SEQUENCE CHARACTERISTICS:
73 (A) LENGTH: 68 base pairs
74 (B) TYPE: nucleic acid
75 (C) STRANDEDNESS: single
76 (D) TOPOLOGY: linear
78 (ii) MOLECULE TYPE: cDNA
80 (iii) HYPOTHETICAL: NO
C--> 82 (iv) ANTI-SENSE: NO
86 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
88 CCGGGGAGGC CTGCACGTGA TCGAGGGCAG ACACCATCAC CACCATCACT AATAGTTAAT 60
90 TAACTGCA 68
92 (2) INFORMATION FOR SEQ ID NO: 3:
94 (i) SEQUENCE CHARACTERISTICS:
95 (A) LENGTH: 642 base pairs
96 (B) TYPE: nucleic acid
97 (C) STRANDEDNESS: single
98 (D) TOPOLOGY: linear
100 (ii) MOLECULE TYPE: cDNA
102 (iii) HYPOTHETICAL: NO
C--> 104 (iv) ANTI-SENSE: NO
107 (ix) FEATURE:
108 (A) NAME/KEY: CDS
109 (B) LOCATION: 1..639
111 (ix) FEATURE:
112 (A) NAME/KEY: mat_peptide
113 (B) LOCATION: 1..636
116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
118 ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA CTG TCC TGT 48
119 Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys
120 1 5 10 15
122 CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG TCC GGG ATG 96
123 Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met
124 20 25 30
126 TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA 144
127 Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala
128 35 40 45
130 GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG 192
131 Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu
132 50 55 60
134 AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG CTC GCA GCT 240
135 Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala
136 65 70 75 80
138 AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC GTC GAT TTG 288
139 Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu
140 85 90 95
142 CTC GTT GGG GCG GCT CTC TGT TCC GCT ATG TAC GTG GGG GAT CTC 336
143 Leu Val Gly Ala Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu
144 100 105 110
146 TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC TCG CCT CGC 384

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147	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	
148		115			120						125						
150	CGG	CAT	GAG	ACG	GTG	CAG	GAC	TGC	AAT	TGC	ATC	TAT	CCC	GGC	CAC	432	
151	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	
152		130			135						140						
154	ATA	ACA	GGT	CAC	CGT	ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	TGG	TCG	CCT	480
155	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	
156	145			150						155			160				
158	ACA	ACG	GCC	CTG	GTG	GTA	TCG	CAG	CTG	CTC	CGG	ATC	CCA	CAA	GCT	GTC	528
159	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	
160				165					170			175					
162	GTG	GAC	ATG	GTG	GCG	GGG	GCC	CAT	TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	576
163	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	
164		180			185					190							
166	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	GTG	ATG	CTA	624
167	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Ile	Val	Met	Leu	
168		195			200					205							
170	CTC	TTT	GCT	CTC	TAATAG											642	
171	Leu	Phe	Ala	Leu													
172		210															
175	(2)	INFORMATION FOR SEQ ID NO: 4:															
177		(i)	SEQUENCE CHARACTERISTICS:														
178			(A)	LENGTH: 212 amino acids													
179			(B)	TYPE: amino acid													
180			(D)	TOPOLOGY: linear													
182		(ii)	MOLECULE TYPE: protein														
184		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 4:														
186	Met	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	
187	1				5					10			15				
189	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met	
190			20			25				30							
192	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	
193			35			40				45							
195	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	
196			50			55				60							
198	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	
199	65			70					75			80					
201	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu		
202				85.					90			95					
204	Leu	Val	Gly	Ala	Ala	Leu	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu		
205			100			105				110							
207	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	
208		115			120					125							
210	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	
211		130			135					140							
213	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	
214	145				150					155			160				
216	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	
217				165					170			175					

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219 Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala
 220 180 185 190
 222 Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu
 223 195 200 205
 225 Leu Phe Ala Leu
 226 210

229 (2) INFORMATION FOR SEQ ID NO: 5:

231 (i) SEQUENCE CHARACTERISTICS:
 232 (A) LENGTH: 795 base pairs
 233 (B) TYPE: nucleic acid
 234 (C) STRANDEDNESS: single
 235 (D) TOPOLOGY: linear
 237 (iii) MOLECULE TYPE: cDNA
 239 (iii) HYPOTHETICAL: NO
 C--> 241 (iv) ANTI-SENSE: NO
 244 (ix) FEATURE:
 245 (A) NAME/KEY: CDS
 246 (B) LOCATION: 1..792
 248 (ix) FEATURE:
 249 (A) NAME/KEY: mat_peptide
 250 (B) LOCATION: 1..789

253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

255 ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
256 Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
257 1 5 10 15	
259 GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
260 Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
261 20 25 30	
263 GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
264 Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
265 35 40 45	
267 ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
268 Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Ala Leu	
269 50 55 60	
271 CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
272 Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
273 65 70 75 80	
275 TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
276 Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
277 85 90 95	
279 TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
280 Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
281 100 105 110	
283 GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
284 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
285 115 120 125	
287 CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
288 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	
289 130 135 140	

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291	GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG	480
292	Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val	
293	145 150 155 160	
295	GGG GAC CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC	528
296	Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
297	165 170 175	
299	TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT	576
300	Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	
301	180 185 190	
303	CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC	624
304	Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn	
305	195 200 205	
307	TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA	672
308	Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro	
309	210 215 220	
311	CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG	720
312	Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala	
313	225 230 235 240	
315	GGT CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT	768
316	Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile	
317	245 250 255	
319	GTG ATG CTA CTC TTT GCT CCC TAATAG	795
320	Val Met Leu Leu Phe Ala Pro	
321	260	

324 (2) INFORMATION FOR SEQ ID NO: 6:

326 (i) SEQUENCE CHARACTERISTICS:

327 (A) LENGTH: 263 amino acids

328 (B) TYPE: amino acid

329 (D) TOPOLOGY: linear

331 (ii) MOLECULE TYPE: protein

333 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

335	Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
336	1 5 10 15	
338	Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
339	20 25 30	
341	Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
342	35 40 45	
344	Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
345	50 55 60	
347	Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
348	65 70 75 80	
350	Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
351	85 90 95	
353	Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
354	100 105 110	
356	Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
357	115 120 125	
359	Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	
360	130 135 140	

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/899,303A

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TIME: 18:16:04

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Output Set: N:\CRF3\11232001\I899303A.raw

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L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:61 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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L:104 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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L:399 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:467 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:536 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:587 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
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L:3444 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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